Drosophila Stock Center at Indiana University (Bloomington, IN), a public repository containing about 7000 fly stocks including a variety of deficiency stocks and stocks carrying mutant alleles of particular genes. A complete list of stocks is available on the world wide web at flystocks.bio.indiana.edu.

Please amend the paragraph bridging pages 35 and 36 to read as follows:

Control siblings can be conveniently identified in *Drosophila* using balancer chromosomes. As used herein, the term "balancer chromosome" means a multiply inverted *Drosophila* chromosome usually carrying a dominant marker mutation. One skilled in the art understands that a useful balancer chromosome carries multiple chromosomal inversions and suppresses recombination along the full length of the chromosome. A balancer chromosome also can carry a dominant marker mutation resulting in a phenotype such as a particular eye color or wing phenotype that can be readily identified in flies carrying the balancer. In addition, a balancer chromosome may contain one or more recessive marker mutations for easy identification of progeny carrying two copies of the balancer during segregation analysis. Balancer chromosomes are available for the X, second, and third *Drosophila* chromosomes: for example, *FM7a*, *FM7b* and *FM7c* are convenient X chromosome balancers; *SM6* and *In(2LR)O, Cy dp^{lvl} pr cn^2* are convenient balancers for the second chromosome; and *TM3, TM6, TM6B* and *TM8* are convenient balancers for the third chromosome. Balancer chromosomes can be obtained from The

Bloomington *Drosophila* Stock Center at Indiana University. A
complete list of available balancer chromosomes is available on
the world wide web at flystocks.bio.indiana.edu. Methods of
constructing stocks utilizing balancer chromosomes are well known
in the art as described, for example, in Greenspan, *supra*, 1997.

Please amend the paragraph bridging pages 64 and 65 to read as
follows:

Sequence analysis using the BLAST program on the world
wide web at either the Berkeley *Drosophila* Genome Project
website or at the NCBI website revealed that about 15% of the
transcripts represented sequences currently available in
Drosophila databases (Table 4). In particular, the following
genes were identified with altered RNA expression levels in *Appl^d*
flies. *Shibire* (*shi*), which encodes dynamin (van der Bliek and
Meyerowitz, Nature 351:411-414 (1991)); *cap-n-collar* (*cnc*), which
encodes a bZIP-like transcription factor (Mohler et al., Mech.
Dev. 34:3-9 (1991)), *Pbprp-2*, which encodes a
pheromone-binding-protein-related-protein (Pikielny et al.,
Neuron 12:35-49 (1994)); *RpL9*, encoding ribosomal protein L9
(Schmidt et al., Mol. Gen. Genet. 251:381-387 (1996)); *Dhod*
(Jones et al., Mol. Gen. Genet. 219:397-403 (1989)), 18S
ribosomal RNA; *Tat-binding protein-1 (Tbp-1*, FlyBase FBgn0026321)
of the proteasome; and a homolog of rat *exo84* of the exocyst
secretion complex (Kee et al., Proc. Natl. Acad. Sci. USA
94:14438-14443 (1997)).

Please amend the paragraph at page 65, lines 7-20 to read as follows:

mRNA levels also were compared using a DNA microarray made from 400 randomly chosen ESTs from the Berkeley *Drosophila* Genome Project UniGene Library, which can be found on the world wide web. Briefly, a glass slide DNA microarray was prepared as described in White et al., Science 286:2179-2184 (1999), from the UniGene Library (plates #54, 55, 56 and 57; Research Genetics, Huntsville, AL). PolyA+ RNA was prepared from groups of 100 whole flies using MicroPoly(A)Pure (Ambion, Austin, TX) according to the manufacturer's instructions, and subsequently labeled and hybridized to the arrays as described in White et al., *supra,* 1999. ESTs showing >2-fold expression difference were analyzed as described above.

REMARKS

As requested in the Office communication mailed June 3, 2003 (Paper No. 15), Applicants have amended the specification to remove hyperlinks and other forms of browser-executable code. The amendments to the specification do not add any new subject matter and entry of the amendments is respectfully requested.

Applicants have set forth above the amendment to specification in clean form as required under 37 C.F.R.